Amendments to the Specification:

Please replace the paragraph beginning at page 13, line 10 with the following amended paragraph:

Methods of the invention allow for multiplexed reactions, e.g., reactions in which two or more targets, and preferably as many as 10, 50, 100, 200, 500, 1000, or 5000 target sequences, are analyzed. Targets can be on the same molecule or can be on different molecules. In the examples below an embodiment wherein the targets are on different molecules is described, but the method can be used to analyze different regions of a single molecule. Thus, in a preferred embodiment the reaction mix includes a second target, and a third and a forth probe are included in the reaction mix, wherein said third probe includes, preferably in the order of 5' to 3', a first region which includes a universal primer sequence; a second region which includes a capture tag sequence (which is preferably different form the capture tag sequence on one or both of the first and second probe) and a cleavage site, e.g., a site for cleavage by a restriction enzyme, and a third region which can which can hybridize to a first region on the target nucleic acid, wherein said fourth probe includes, preferably in the order of 5' to 3', a first region which can which can hybridize to a second region on the target nucleic acid (the first and second region of the target sequence can abut, or can be separated by 1 or **[[____]]** **more** nucleotides, in the case where the regions about, the third and fourth probe can be joined by ligation, in the case where they are separated by one or more nucleotides the third and fourth probe/primer can be joined by polymerase directed synthesis and ligation), a second region which includes a capture tag sequence (which is preferably different form the capture tag sequence on one or both of the first and second primer, and which can be the same or different, and is preferably of different sequence, from that of the capture tag of the third primer) and a cleavage site, e.g., a site for cleavage by a restriction enzyme, and a third region which includes a universal primer sequence; forming a reaction mixture which includes the first, second, third and fourth probe and the two targets under conditions wherein the third and fourth probe are joined, e.g., by ligation, if the

second target is of a first sequence and not joined if the second target is of a second sequence, to produce a second joined probe/primer, which preferably includes, in order, a universal primer sequence, a capture tag sequence, target sequence, a capture tag sequence, and a universal primer sequence, preferably in the order 5' to 3'; optionally, contacting a second joined probe with a pair of universal primers which bind to the universal primer sequences (and preferably not to regions on the second joined probe other than the universal primer sequences) and extending the universal primers along the second joined probe strand (or its complement) to produce one or a plurality of double stranded molecules having, in order, a universal primer sequence, a capture tag sequence, second target sequence, a capture tag sequence, and a universal primer sequence; **and** cleaving at the cleavage site of one or both ends of a double strand joined probe to provide a derivative nucleic acid which is a double stranded molecule having overhangs which include the capture tag sequence at one or both of the 3' and 5' termini, preferably at the 3' terminus **[[,]]** .